Attorney Docket: 2055GG/48747TR
PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	GUY A. ROULEAU ET AL.		
Serial No.:	09/508,821	Group Art Unit:	1655
Filed:	MAY 26, 2000	Examiner:	J. GOLDBERG
Title:	POLYMORPHIC CAG REPEAT-CONTAINING GENE AND USES THEREOF		

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11/9/01

AMENDMENT

Box Fee Amendment
Commissioner for Patents
Washington, D.C. 20231

Sir:

This Amendment is in response to the Official Action mailed May 9, 2001. A Petition for Extension of Time is filed concurrently herewith. Please amend the application as follows:

IN THE SPECIFICATION:

Please amend the paragraph beginning on page 16, line 16 and continuing to page 17, line 7 as follows:

Sub D1 C

Only allelic variants of the GCT10D04 locus (primers; SCZ15:GGGGCAGCGGGTCCAGAATCTTC (SEQ. ID NO: 3), SCZ16: TCGCCTTGCTGCCCGTAGTGCT (SEQ. ID NO: 11); annealing temperature 62°C) showed an overall significant group effect for the L allele (Kruskal-Wallis H (2, N= 194) = 12.18, p = .002), the CAG repeat average length being the shortest in the neuroleptic-responders (Rs), intermediate in the non-responders (NRs) and longest in the control group (C) (Fig. 1).

IN THE CLAIMS:

Please cancel claims 6-8 and 12 without prejudice or disclaimer of the subject matter therein. Please amend the claims and add new claims as follows:

sub D2 C2

1. (Amended) An isolated human hGT1 gene comprising a transcribed polymorphic CAG repeat having the sequence $(CAU)_2(CAG)_nCAA$, wherein U is A or G and n is from 7 to 12, wherein allelic variants of said CAG repeat are associated with a disorder selected from the group consisting of psychiatric diseases, schizophrenia, affective disorders, neurodevelopmental brain diseases and phenotypic variability with respect to long term response to neuroleptic medication, and wherein n being equal to 11 is the most common allele of the hGT1 gene.

3. (Amended) A method for evaluating the severity of schizophrenia of a patient, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1,

sub D3 C3

wherein allelic variants shorter than allele 0, which corresponds to n=11, are indicative of less severe schizophrenia in the patient.

4. (Amended) A method for the identification of the response of a patient to neuroleptic medication, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1,

wherein allelic variants shorter than allele 0, which corresponds to n=11, are indicative of a neuroleptic response by said patient.

5. (Amended) The method of claim 4, wherein said shorter allelic variants have a n equal to 8, 9 or 10.

9. (Amended) A method of categorizing a psychiatric patient according to its genotype in order to maximize its response to treatment to at least one neuroleptic drug, which comprises the steps of:

a) obtaining a nucleic acid sample of said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1, wherein a patient is categorized with respect to his allelic variants, and wherein allelic variants shorter than allele 0, which corresponds to n=11, are indicative of a neuroleptic response of said patient.

10. (Amended) A method of identifying a patient which is responsive to a neuroleptic medication which comprises:

a) obtaining a sample from said patient; and

b) determining allelic variants of said CAG repeat of the gene of claim 1, wherein allelic variants shorter than allele 0, which corresponds to n=11, identify said patient as a neuroleptic responder.

11. (Amended) The method of claim 10, wherein said sample is a nucleic acid sample and wherein shorter allelic variants have a n equal to 8, 9 or 10.

13. (New) The human gene of claim 1, wherein n is selected from the group consisting of 7, 8, 9, 10 and 12, and wherein said allelic variant is associated with schizophrenia.

14. (New) The human gene of claim 13, wherein n is selected from:

a) n is 7 to 10, wherein said allelic variant is associated with a neuroleptic medication-responsive status of a schizophrenic patient, and

b) n is equal to 12, wherein said allelic variant is associated with a poor responsive status of a schizophrenic patient to neuroleptic medication.

15. (New) The human gene of claim 1, wherein n is equal to 11, which comprises the sequence as set forth in SEQ ID NO:2.

16. (New) The human gene of claim 15 comprising the sequence as set forth in SEQ ID NO:5.

17. (New) An isolated nucleic acid sequence comprising the sequence as set forth in SEQ ID NO:2.

18. (New) The isolated nucleic acid sequence of claim 17 comprising the sequence as set forth in SEQ ID NO:5.

19. (New) An isolated nucleic acid sequence comprising a sequence encoding the amino acid sequence as set forth in SEQ ID NO:6.

20. (New) A vector which expresses the isolated nucleic acid sequence of claim 17.

21. (New) A vector which expresses the isolated nucleic acid sequence of claim 18.

22. (New) A vector which expresses the gene of claim 1.

23. (New) A cell harboring the vector of claim 20.

24. (New) A cell harboring the vector of claim 21.

25. (New) A cell harboring the vector of claim 22.

IN THE ABSTRACT:

Following the claims, please add an abstract of the disclosure as provided on an attached, separate sheet.

REMARKS

Responsive to the restriction requirement, Applicants elect Group I, Claims 1-5 a 9-11. By the above-noted amendments, Applicants further clarify the claimed subj matter of Group I by presenting amendments to the elected claims, and by presenting n claims to more particularly point out and distinctly claim the elected subject matter. Th is no new matter presented by this amendment.

Applicants provide concurrently herewith a second substituted sequence listing w computer-readable copy and a Statement under 35 C.F.R. §1.821(f). The second substit sequence listing is provided to show the hGT1 amino acid sequence. The pertinent port of SEQ ID NO:5 has been translated, this being the only difference between the seco substitute sequence listing presented herewith and the substitute sequence listing January 24, 2001. Support for the translation of SEQ ID NO:5 can be found in specification at page 8, lines 30-32, describing the 5535 bp open reading frame. Supp can also be found at page 8, line 35 to page 9, line 2, describing the 490 bp intron preced the ORF.

Support for the amendment to claim 1 can be found at page 9, line 15, and in S ID NO:2, showing the selection of U and the range of potential values for n. Support the amendment to claims 3 and 4 can be found at page 19, lines 3-5 and page 21, lines 3 discussing the correlation between n and the severity of dysfunction or disease. Supp for the amendment to claim 5 can be found at page 4, lines 20-23, showing the variety values for n. Support for the amendment to claim 9 can be found at page 10, lines 3- discussing the use of neuroleptic drugs. Support for the amendment to claim 10 can

found in the originally filed claims and in the disclosure. Support for the amendment claim 11 can be found at page 4, lines 20-23, showing the range of n values.

Support for new claims 13-25 can be found in the disclosure and claims as originally filed. Specific support for claims 20-25 can be found at page 5, line 35 to page 6, line 3.

If there are any questions regarding this amendment or the application in general, a telephone call to the undersigned would be appreciated since this should expedite the prosecution of the application for all concerned.

If necessary to effect a timely response, this paper should be considered as a petition for an Extension of Time sufficient to effect a timely response, and please charge any deficiency in fees or credit any overpayments to Deposit Account No. 05-1323 (Docket #2055GG/48747TR).

Respectfully submitted,

November 9, 2001

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